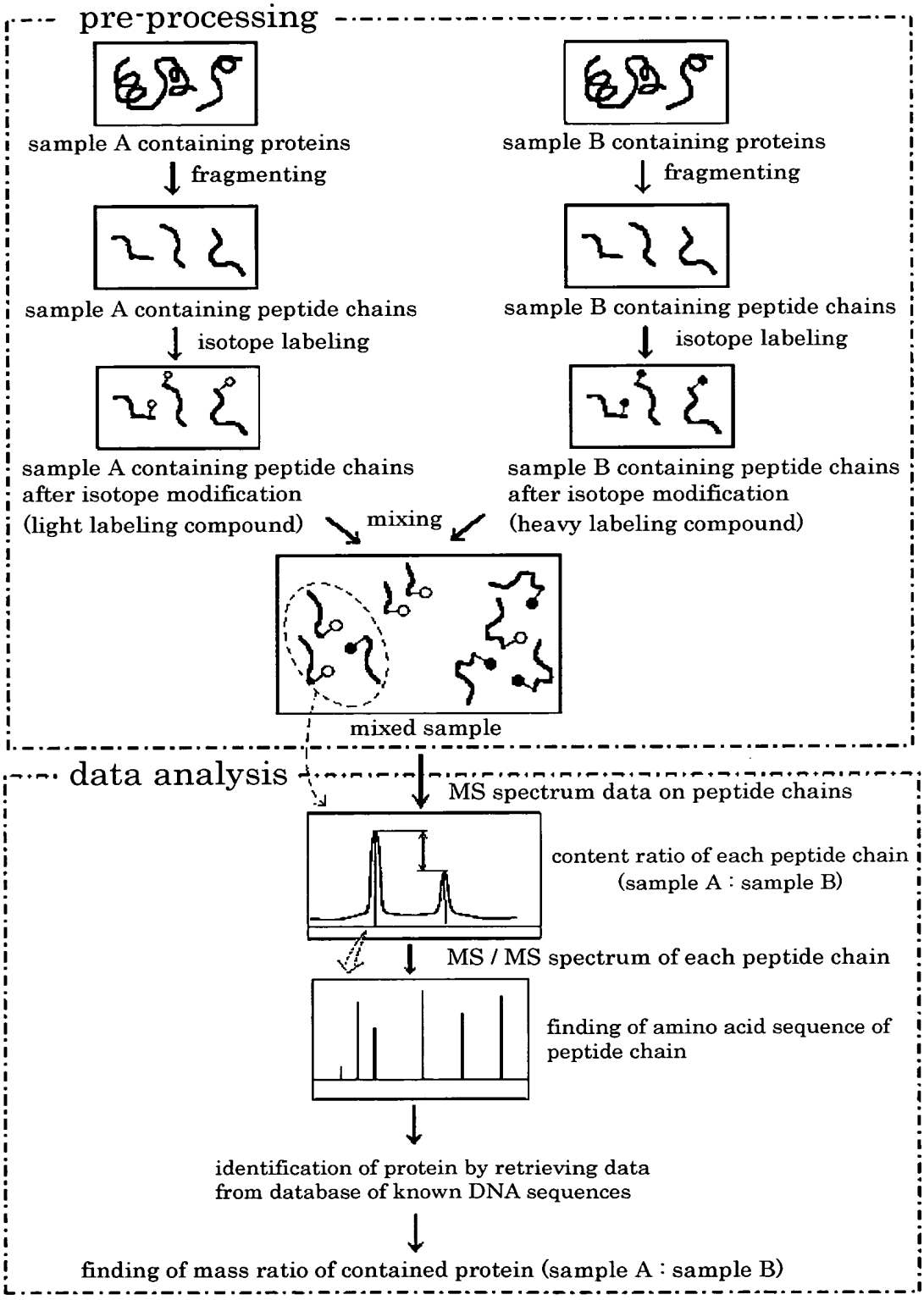
FIG.1


pre-processing
sample A containing proteins
fragmenting
sample A containing peptide chains
isotope labeling
sample A containing peptide chains
after isotope modification
(light labeling compound)
sample B containing proteins
fragmenting
sample B containing peptide chains
isotope labeling
sample B containing peptide chains
after isotope modification
(heavy labeling compound)
mixing
mixed sample
data analysis
MS spectrum data on peptide chains
content ratio of each peptide chain
(sample A : sample B)
MS / MS spectrum of each peptide chain
finding of amino acid sequence of
peptide chain
identification of protein by retrieving data
from database of known DNA sequences
finding of mass ratio of contained protein (sample A : sample B)

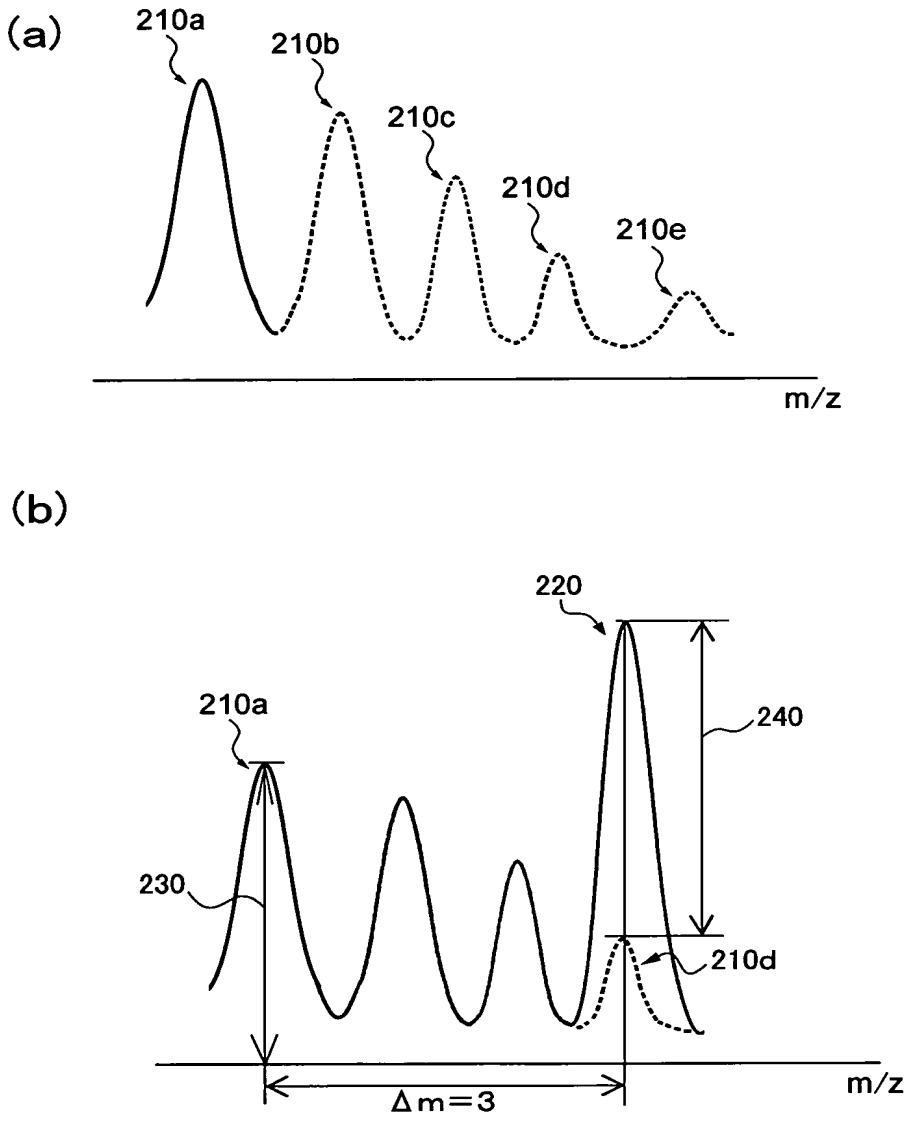



FIG.2